



SEQUENCE LISTING

<110> M&E Biotech A/S

① <120> Method for down-regulating GDF-8 activity

<130> 3631-0117P

<140> 09/620,586

<141> 2000-07-20

<160> 24

<170> PatentIn Ver. 2.1

<210> 1

<211> 375

<212> PRT

<213> Homo sapiens

<400> 1

Met Gln Lys Leu Gln Leu Cys Val Tyr Ile Tyr Leu Phe Met Leu Ile
1 5 10 15
Val Ala Gly Pro Val Asp Leu Asn Glu Asn Ser Glu Gln Lys Glu Asn
20 25 30
Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Thr Trp Arg Gln Asn Thr
35 40 45
Lys Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu
50 55 60
Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Val Ile Arg Gln Leu
65 70 75 80
Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val
85 90 95
Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His
100 105 110
Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu
115 120 125
Met Gln Val Asp Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser
130 135 140
Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu
145 150 155 160
Arg Pro Val Glu Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu
165 170 175
Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu
180 185 190
Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val
195 200 205
Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly
210 215 220
Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr
225 230 235 240
Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Lys
245 250 255
Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys
260 265 270
Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val

275	280	285	
Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr			
290	295	300	
Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys			
305	310	315	320
Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala			
325	330	335	
Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr			
340	345	350	
Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val			
355	360	365	
Val Asp Arg Cys Gly Cys Ser			
370	375		

<210> 2
 <211> 362
 <212> PRT
 <213> Meleagris gallopavo

<400> 2

Met Gln Ile Leu Val His Pro Val Ala Leu Asp Gly Ser Ser Gln Pro			
1	5	10	15
Thr Glu Asn Ala Glu Lys Asp Gly Leu Cys Asn Ala Cys Thr Trp Arg			
20	25	30	
Gln Asn Thr Lys Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu			
35	40	45	
Ser Lys Leu Arg Leu Glu Gln Ala Pro Asn Ile Ser Arg Asp Val Ile			
50	55	60	
Lys Gln Leu Leu Pro Lys Ala Pro Pro Leu Gln Glu Leu Ile Asp Gln			
65	70	75	80
Tyr Asp Val Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp			
85	90	95	
Asp Tyr His Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser			
100	105	110	
Asp Phe Leu Val Gln Met Glu Gly Lys Pro Lys Cys Cys Phe Phe Lys			
115	120	125	
Phe Ser Ser Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp			
130	135	140	
Ile Tyr Leu Arg Gln Val Gln Lys Pro Thr Thr Val Phe Val Gln Ile			
145	150	155	160
Leu Arg Leu Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile			
165	170	175	
Arg Ser Leu Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser			
180	185	190	
Ile Asp Val Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser			
195	200	205	
Asn Leu Gly Ile Glu Ile Lys Ala Phe Asp Glu Asn Gly Arg Asp Leu			
210	215	220	
Ala Val Thr Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu			
225	230	235	240
Glu Val Arg Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly			
245	250	255	
Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro			
260	265	270	
Leu Thr Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro			
275	280	285	

Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe
 290 295 300
 Leu Gln Lys Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg
 305 310 315 320
 Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn
 325 330 335
 Met Leu Tyr Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro
 340 345 350
 Ala Met Val Val Asp Arg Cys Gly Cys Ser
 355 360

<210> 3
 <211> 375
 <212> PRT
 <213> Gallus sp.

<400> 3

Met Gln Lys Leu Ala Val Tyr Val Tyr Ile Tyr Leu Phe Met Gln Ile
 1 5 10 15
 Ala Val Asp Pro Val Ala Leu Asp Gly Ser Ser Gln Pro Thr Glu Asn
 20 25 30
 Ala Glu Lys Asp Gly Leu Cys Asn Ala Cys Thr Trp Arg Gln Asn Thr
 35 40 45
 Lys Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu
 50 55 60
 Arg Leu Glu Gln Ala Pro Asn Ile Ser Arg Asp Val Ile Lys Gln Leu
 65 70 75 80
 Leu Pro Lys Ala Pro Pro Leu Gln Glu Leu Ile Asp Gln Tyr Asp Val
 85 90 95
 Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His
 100 105 110
 Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu
 115 120 125
 Val Gln Met Glu Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser
 130 135 140
 Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu
 145 150 155 160
 Arg Gln Val Gln Lys Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu
 165 170 175
 Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu
 180 185 190
 Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val
 195 200 205
 Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly
 210 215 220
 Ile Glu Ile Lys Ala Phe Asp Glu Thr Gly Arg Asp Leu Ala Val Thr
 225 230 235 240
 Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Arg
 245 250 255
 Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys
 260 265 270
 Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val
 275 280 285
 Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr
 290 295 300
 Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys

305	310	315	320
Tyr Pro His Thr His	Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala		
325	330	335	
Gly Pro Cys Cys	Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr		
340	345	350	
Phe Asn Gly Lys Glu Gln Ile	Ile Tyr Gly Lys Ile Pro Ala Met Val		
355	360	365	
Val Asp Arg Cys Gly Cys Ser			
370	375		

<210> 4

<211> 376

<212> PRT

<213> Mus musculus

<400> 4

Met Met Gln Lys Leu Gln Met Tyr Val Tyr Ile Tyr Leu Phe Met Leu			
1	5	10	15
Ile Ala Ala Gly Pro Val Asp Leu Asn Glu Gly Ser Glu Arg Glu Glu			
20	25	30	
Asn Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Ala Trp Arg Gln Asn			
35	40	45	
Thr Arg Tyr Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys			
50	55	60	
Leu Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln			
65	70	75	80
Leu Leu Pro Arg Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp			
85	90	95	
Val Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr			
100	105	110	
His Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe			
115	120	125	
Leu Met Gln Ala Asp Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser			
130	135	140	
Ser Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr			
145	150	155	160
Leu Arg Pro Val Lys Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg			
165	170	175	
Leu Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser			
180	185	190	
Leu Lys Leu Asp Met Ser Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp			
195	200	205	
Val Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu			
210	215	220	
Gly Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val			
225	230	235	240
Thr Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val			
245	250	255	
Lys Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp			
260	265	270	
Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr			
275	280	285	
Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg			
290	295	300	
Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln			
305	310	315	320

Lys	Tyr	Pro	His	Thr	His	Leu	Val	His	Gln	Ala	Asn	Pro	Arg	Gly	Ser
						325			330					335	
Ala	Gly	Pro	Cys	Cys	Thr	Pro	Thr	Lys	Met	Ser	Pro	Ile	Asn	Met	Leu
						340			345					350	
Tyr	Phe	Asn	Gly	Lys	Glu	Gln	Ile	Ile	Tyr	Gly	Lys	Ile	Pro	Ala	Met
						355			360					365	
Val	Val	Asp	Arg	Cys	Gly	Cys	Ser								
						370			375						

<210> 5
 <211> 375
 <212> PRT
 <213> Bos taurus

<400> 5															
Met	Gln	Lys	Leu	Gln	Ile	Ser	Val	Tyr	Ile	Tyr	Leu	Phe	Met	Leu	Ile
1			5						10				15		
Val	Ala	Gly	Pro	Val	Asp	Leu	Asn	Glu	Asn	Ser	Glu	Gln	Lys	Glu	Asn
									20			25		30	
Val	Glu	Lys	Glu	Gly	Leu	Cys	Asn	Ala	Cys	Leu	Trp	Arg	Glu	Asn	Thr
									35			40		45	
Thr	Ser	Ser	Arg	Leu	Glu	Ala	Ile	Lys	Ile	Gln	Ile	Leu	Ser	Lys	Leu
									50			55		60	
Arg	Leu	Glu	Thr	Ala	Pro	Asn	Ile	Ser	Lys	Asp	Ala	Ile	Arg	Gln	Leu
									65			70		75	
Leu	Pro	Lys	Ala	Pro	Pro	Leu	Leu	Glu	Leu	Ile	Asp	Gln	Phe	Asp	Val
									85			90		95	
Gln	Arg	Asp	Ala	Ser	Ser	Asp	Gly	Ser	Leu	Glu	Asp	Asp	Asp	Tyr	His
									100			105		110	
Ala	Arg	Thr	Glu	Thr	Val	Ile	Thr	Met	Pro	Thr	Glu	Ser	Asp	Leu	Leu
									115			120		125	
Thr	Gln	Val	Glu	Gly	Lys	Pro	Lys	Cys	Cys	Phe	Phe	Lys	Phe	Ser	Ser
									130			135		140	
Lys	Ile	Gln	Tyr	Asn	Lys	Leu	Val	Lys	Ala	Gln	Leu	Trp	Ile	Tyr	Leu
									145			150		155	
Arg	Pro	Val	Lys	Thr	Pro	Ala	Thr	Val	Phe	Val	Gln	Ile	Leu	Arg	Leu
									165			170		175	
Ile	Lys	Pro	Met	Lys	Asp	Gly	Thr	Arg	Tyr	Thr	Gly	Ile	Arg	Ser	Leu
									180			185		190	
Lys	Leu	Asp	Met	Asn	Pro	Gly	Thr	Gly	Ile	Trp	Gln	Ser	Ile	Asp	Val
									195			200		205	
Lys	Thr	Val	Leu	Gln	Asn	Trp	Leu	Lys	Gln	Pro	Glu	Ser	Asn	Leu	Gly
									210			215		220	
Ile	Glu	Ile	Lys	Ala	Leu	Asp	Glu	Asn	Gly	His	Asp	Leu	Ala	Val	Thr
									225			230		235	
Phe	Pro	Glu	Pro	Gly	Glu	Asp	Gly	Leu	Thr	Pro	Phe	Leu	Glu	Val	Lys
									245			250		255	
Val	Thr	Asp	Thr	Pro	Lys	Arg	Ser	Arg	Arg	Asp	Phe	Gly	Leu	Asp	Cys
									260			265		270	
Asp	Glu	His	Ser	Thr	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr	Val
									275			280		285	
Asp	Phe	Glu	Ala	Phe	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Arg	Tyr
									290			295		300	
Lys	Ala	Asn	Tyr	Cys	Ser	Gly	Glu	Cys	Glu	Phe	Val	Phe	Leu	Gln	Lys
									305			310		315	
Tyr	Pro	His	Thr	His	Leu	Val	His	Gln	Ala	Asn	Pro	Arg	Gly	Ser	Ala

	325	330	335
Gly Pro Cys Cys	Thr Pro Thr Lys	Met Ser Pro Ile Asn	Met Leu Tyr
340	345	350	
Phe Asn Gly Glu Gly Gln	Ile Ile Tyr Gly Lys	Ile Pro Ala Met Val	
355	360	365	
Val Asp Arg Cys Gly Cys Ser			
370	375		

<210> 6
 <211> 375
 <212> PRT
 <213> Ovis sp.

<400> 6			
Met Gln Lys Leu Gln Ile Phe Val Tyr Ile Tyr Leu Phe Met Leu Leu			
1	5	10	15
Val Ala Gly Pro Val Asp Leu Asn Glu Asn Ser Glu Gln Lys Glu Asn			
20	25	30	
Val Glu Lys Lys Gly Leu Cys Asn Ala Cys Leu Trp Arg Gln Asn Asn			
35	40	45	
Lys Ser Ser Arg Leu Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu			
50	55	60	
Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln Leu			
65	70	75	80
Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val			
85	90	95	
Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His			
100	105	110	
Val Thr Thr Glu Thr Val Ile Thr Met Pro Thr Glu Ser Asp Leu Leu			
115	120	125	
Ala Glu Val Gln Glu Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser			
130	135	140	
Lys Ile Gln His Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu			
145	150	155	160
Arg Pro Val Lys Thr Pro Thr Val Phe Val Gln Ile Leu Arg Leu			
165	170	175	
Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu			
180	185	190	
Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val			
195	200	205	
Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly			
210	215	220	
Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr			
225	230	235	240
Phe Pro Glu Pro Gly Glu Glu Gly Leu Asn Pro Phe Leu Glu Val Lys			
245	250	255	
Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys			
260	265	270	
Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val			
275	280	285	
Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr			
290	295	300	
Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Leu Phe Leu Gln Lys			
305	310	315	320
Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Lys Gly Ser Ala			
325	330	335	

Gly	Pro	Cys	Cys	Thr	Pro	Thr	Lys	Met	Ser	Pro	Ile	Asn	Met	Leu	Tyr
340							345						350		
Phe	Asn	Gly	Lys	Glu	Gln	Ile	Ile	Tyr	Gly	Lys	Ile	Pro	Gly	Met	Val
355						360							365		
Val	Asp	Arg	Cys	Gly	Cys	Ser									
370						375									

<210> 7
 <211> 376
 <212> PRT
 <213> Rattus norvegicus

<400> 7
 Met Ile Gln Lys Pro Gln Met Tyr Val Tyr Ile Tyr Leu Phe Val Leu
 1 5 10 15
 Ile Ala Ala Gly Pro Val Asp Leu Asn Glu Asp Ser Glu Arg Glu Ala
 20 25 30
 Asn Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Ala Trp Arg Gln Asn
 35 40 45
 Thr Arg Tyr Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys
 50 55 60
 Leu Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln
 65 70 75 80
 Leu Leu Pro Arg Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp
 85 90 95
 Val Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr
 100 105 110
 His Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe
 115 120 125
 Leu Met Gln Ala Asp Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser
 130 135 140
 Ser Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr
 145 150 155 160
 Leu Arg Ala Val Lys Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg
 165 170 175
 Leu Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser
 180 185 190
 Leu Lys Leu Asp Met Ser Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp
 195 200 205
 Val Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu
 210 215 220
 Gly Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val
 225 230 235 240
 Thr Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val
 245 250 255
 Lys Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp
 260 265 270
 Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr
 275 280 285
 Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg
 290 295 300
 Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln
 305 310 315 320
 Lys Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser
 325 330 335
 Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu

	340	345	350												
Tyr	Phe	Asn	Gly	Lys	Glu	Gln	Ile	Ile	Tyr	Gly	Lys	Ile	Pro	Ala	Met
	355						360					365			
Val	Val	Asp	Arg	Cys	Gly	Cys	Ser								
	370					375									

<210> 8
 <211> 375
 <212> PRT
 <213> Sus scrofa

<400> 8

Met	Gln	Lys	Leu	Gln	Ile	Tyr	Val	Tyr	Ile	Tyr	Leu	Phe	Met	Leu	Ile
1			5						10				15		
Val	Ala	Gly	Pro	Val	Asp	Leu	Asn	Glu	Asn	Ser	Glu	Gln	Lys	Glu	Asn
								20		25			30		
Val	Glu	Lys	Glu	Gly	Leu	Cys	Asn	Ala	Cys	Met	Trp	Arg	Gln	Asn	Thr
								35		40		45			
Lys	Ser	Ser	Arg	Leu	Glu	Ala	Ile	Lys	Ile	Gln	Ile	Leu	Ser	Lys	Leu
								50		55		60			
Arg	Leu	Glu	Thr	Ala	Pro	Asn	Ile	Ser	Lys	Asp	Ala	Ile	Arg	Gln	Leu
	65							70			75		80		
Leu	Pro	Lys	Ala	Pro	Pro	Leu	Arg	Glu	Leu	Ile	Asp	Gln	Tyr	Asp	Val
								85		90		95			
Gln	Arg	Asp	Asp	Ser	Ser	Asp	Gly	Ser	Leu	Glu	Asp	Asp	Tyr	His	
								100		105		110			
Ala	Thr	Thr	Glu	Thr	Ile	Ile	Thr	Met	Pro	Thr	Glu	Ser	Asp	Leu	Leu
								115		120		125			
Met	Gln	Val	Glu	Gly	Lys	Pro	Lys	Cys	Cys	Phe	Phe	Lys	Phe	Ser	Ser
								130		135		140			
Lys	Ile	Gln	Tyr	Asn	Lys	Val	Val	Lys	Ala	Gln	Leu	Trp	Ile	Tyr	Leu
	145							150			155		160		
Arg	Pro	Val	Lys	Thr	Pro	Thr	Thr	Val	Phe	Val	Gln	Ile	Leu	Arg	Leu
								165		170		175			
Ile	Lys	Pro	Met	Lys	Asp	Gly	Thr	Arg	Tyr	Thr	Gly	Ile	Arg	Ser	Leu
								180		185		190			
Lys	Leu	Asp	Met	Asn	Pro	Gly	Thr	Gly	Ile	Trp	Gln	Ser	Ile	Asp	Val
								195		200		205			
Lys	Thr	Val	Leu	Gln	Asn	Trp	Leu	Lys	Gln	Pro	Glu	Ser	Asn	Leu	Gly
								210		215		220			
Ile	Glu	Ile	Lys	Ala	Leu	Asp	Glu	Asn	Gly	His	Asp	Leu	Ala	Val	Thr
	225							230			235		240		
Phe	Pro	Gly	Pro	Gly	Glu	Asp	Gly	Leu	Asn	Pro	Phe	Leu	Glu	Val	Lys
								245		250		255			
Val	Thr	Asp	Thr	Pro	Lys	Arg	Ser	Arg	Arg	Asp	Phe	Gly	Leu	Asp	Cys
								260		265		270			
Asp	Glu	His	Ser	Thr	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr	Val
								275		280		285			
Asp	Phe	Glu	Ala	Phe	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Arg	Tyr
	290							295			300				
Lys	Ala	Asn	Tyr	Cys	Ser	Gly	Glu	Cys	Glu	Phe	Val	Phe	Leu	Gln	Lys
	305							310			315		320		
Tyr	Pro	His	Thr	His	Leu	Val	His	Gln	Ala	Asn	Pro	Arg	Gly	Ser	Ala
								325		330		335			
Gly	Pro	Cys	Cys	Thr	Pro	Thr	Lys	Met	Ser	Pro	Ile	Asn	Met	Leu	Tyr
								340		345		350			

Phe	Asn	Gly	Lys	Glu	Gln	Ile	Ile	Tyr	Gly	Lys	Ile	Pro	Ala	Met	Val
355						360					365				
Val	Asp	Arg	Cys	Gly	Cys	Ser									
370						375									

<210> 9
<211> 374
<212> PRT
<213> Danio rerio

<400> 9

Met	His	Phe	Thr	Gln	Val	Leu	Ile	Ser	Leu	Ser	Val	Leu	Ile	Ala	Cys
1					5				10				15		
Gly	Pro	Val	Gly	Tyr	Gly	Asp	Ile	Thr	Ala	His	Gln	Gln	Pro	Ser	Thr
					20			25					30		
Ala	Thr	Glu	Glu	Ser	Glu	Leu	Cys	Ser	Thr	Cys	Glu	Phe	Arg	Gln	His
					35			40				45			
Ser	Lys	Leu	Met	Arg	Leu	His	Ala	Ile	Lys	Ser	Gln	Ile	Leu	Ser	Lys
					50			55				60			
Leu	Arg	Leu	Lys	Gln	Ala	Pro	Asn	Ile	Ser	Arg	Asp	Val	Val	Lys	Gln
					65			70				75			80
Leu	Leu	Pro	Lys	Ala	Pro	Pro	Leu	Gln	Gln	Leu	Leu	Asp	Gln	Tyr	Asp
					85					90				95	
Val	Leu	Gly	Asp	Asp	Ser	Lys	Asp	Gly	Ala	Val	Glu	Glu	Asp	Asp	Glu
					100			105				110			
His	Ala	Thr	Thr	Glu	Thr	Ile	Met	Thr	Met	Ala	Thr	Glu	Pro	Asp	Pro
					115			120				125			
Ile	Val	Gln	Val	Asp	Arg	Lys	Pro	Lys	Cys	Cys	Phe	Phe	Ser	Phe	Ser
					130			135				140			
Pro	Lys	Ile	Gln	Ala	Asn	Arg	Ile	Val	Arg	Ala	Gln	Leu	Trp	Val	His
					145			150				155			160
Leu	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Thr	Val	Phe	Leu	Gln	Ile	Ser	Arg
					165				170				175		
Leu	Met	Pro	Val	Lys	Asp	Gly	Gly	Arg	His	Arg	Ile	Arg	Ser	Leu	Lys
					180			185				190			
Ile	Asp	Val	Asn	Ala	Gly	Val	Thr	Ser	Trp	Gln	Ser	Ile	Asp	Val	Lys
					195			200				205			
Gln	Val	Leu	Thr	Val	Trp	Leu	Lys	Gln	Pro	Glu	Thr	Asn	Arg	Gly	Ile
					210			215				220			
Glu	Ile	Asn	Ala	Tyr	Asp	Ala	Lys	Gly	Asn	Asp	Leu	Ala	Val	Thr	Ser
					225			230				235			240
Thr	Glu	Thr	Gly	Glu	Asp	Gly	Leu	Leu	Pro	Phe	Met	Glu	Val	Lys	Ile
					245				250				255		
Ser	Glu	Gly	Pro	Lys	Arg	Ile	Arg	Arg	Asp	Ser	Gly	Leu	Asp	Cys	Asp
					260			265				270			
Glu	Asn	Ser	Ser	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr	Val	Asp
					275			280				285			
Phe	Glu	Asp	Phe	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Arg	Tyr	Lys
					290			295				300			
Ala	Asn	Tyr	Cys	Ser	Gly	Glu	Cys	Asp	Tyr	Met	Tyr	Leu	Gln	Lys	Tyr
					305			310				315			320
Pro	His	Thr	His	Leu	Val	Asn	Lys	Ala	Ser	Pro	Arg	Gly	Thr	Ala	Gly
					325				330				335		
Pro	Cys	Cys	Thr	Pro	Thr	Lys	Met	Ser	Pro	Ile	Asn	Met	Leu	Tyr	Phe
					340			345				350			
Asn	Gly	Lys	Glu	Gln	Ile	Ile	Tyr	Gly	Lys	Ile	Pro	Ser	Met	Val	Val

355
Asp Arg Cys Gly Cys Ser
370

360

365

<210> 10
<211> 375
<212> PRT
<213> Papio hamadryas

<400> 10
Met Gln Lys Leu Gln Leu Cys Val Tyr Ile Tyr Leu Phe Met Leu Ile
1 5 10 15
Val Ala Gly Pro Val Asp Leu Asn Glu Asn Ser Glu Gln Lys Glu Asn
20 25 30
Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Thr Trp Arg Gln Asn Thr
35 40 45
Lys Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu
50 55 60
Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln Leu
65 70 75 80
Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val
85 90 95
Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His
100 105 110
Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu
115 120 125
Met Gln Val Asp Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser
130 135 140
Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu
145 150 155 160
Arg Pro Val Glu Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu
165 170 175
Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu
180 185 190
Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val
195 200 205
Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly
210 215 220
Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr
225 230 235 240
Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Lys
245 250 255
Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys
260 265 270
Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val
275 280 285
Asp Phe Glu Ala Leu Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr
290 295 300
Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys
305 310 315 320
Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala
325 330 335
Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr
340 345 350
Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val
355 360 365

Val Asp Arg Cys Gly Cys Ser
370 375

<210> 11
<211> 109
<212> PRT
<213> Homo sapiens

<220>
<221> PEPTIDE
<222> (1)..(109)
<223> Identical to residues 267-375 in SEQ ID NO: 1

<400> 11
Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys
1 5 10 15
Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile
20 25 30
Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu
35 40 45
Phe Val Phe Leu Gln Lys Tyr Pro His Thr His Leu Val His Gln Ala
50 55 60
Asn Pro Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser
65 70 75 80
Pro Ile Asn Met Leu Tyr Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly
85 90 95
Lys Ile Pro Ala Met Val Val Asp Arg Cys Gly Cys Ser
100 105

<210> 12
<211> 109
<212> PRT
<213> Bos taurus

<220>
<221> PEPTIDE
<222> (1)..(109)
<223> Identical to residues 267-375 in SEQ ID NO: 5

<400> 12
Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys
1 5 10 15
Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile
20 25 30
Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu
35 40 45
Phe Val Phe Leu Gln Lys Tyr Pro His Thr His Leu Val His Gln Ala
50 55 60
Asn Pro Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser
65 70 75 80
Pro Ile Asn Met Leu Tyr Phe Asn Gly Glu Gln Ile Ile Tyr Gly
85 90 95
Lys Ile Pro Ala Met Val Val Asp Arg Cys Gly Cys Ser
100 105

<210> 13
<211> 15
<212> PRT
<213> Clostridium tetani

<400> 13
Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu
1 5 10 15

<210> 14
<211> 21
<212> PRT
<213> Clostridium tetani

<400> 14
Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser
1 5 10 15

Ala Ser His Leu Glu
20

<210> 15
<211> 109
<212> PRT
<213> Artificial sequence

<220>
<221> MUTAGEN
<222> (18)..(32)
<223> Tetanus toxoid P2 epitope (SEQ ID NO: 13)

<220>
<221> SIMILAR
<222> (1)..(17)
<223> Identical to residues 267-283 in SEQ ID NO: 1

<220>
<221> SIMILAR
<222> (33)..(109)
<223> Identical to residues 299-375 in SEQ ID NO: 1

<220>
<221> SITE
<222> (73)
<223> Cys or Ser

<220>
<221> SITE
<222> (90)..(91)
<223> Lys Glu or Glu Gly

<400> 15
Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys
1 5 10 15
Arg Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu

20	25	30
Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu		
35	40	45
Phe Val Phe Leu Gln Lys Tyr Pro His Thr His Leu Val His Gln Ala		
50	55	60
Asn Pro Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser		
65	70	75
Pro Ile Asn Met Leu Tyr Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly		
85	90	95
Lys Ile Pro Ala Met Val Val Asp Arg Cys Gly Cys Ser		
100	105	

<210> 16
 <211> 109
 <212> PRT
 <213> Artificial sequence

<220>
 <221> MUTAGEN
 <222> (52)..(66)
 <223> Tetanus toxoid P2 epitope (SEQ ID NO: 13)

<220>
 <221> SIMILAR
 <222> (1)..(51)
 <223> Identical to residues 267-317 in SEQ ID NO: 1

<220>
 <221> SIMILAR
 <222> (67)..(109)
 <223> Identical to residues 333-375 in SEQ ID NO: 1

<220>
 <221> SITE
 <222> (73)
 <223> Cys or Ser

<220>
 <221> SITE
 <222> (90)..(91)
 <223> Lys Glu or Glu Gly

<400> 16

Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys			
1	5	10	15
Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile			
20	25	30	
Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu			
35	40	45	
Phe Val Phe Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr			
50	55	60	
Glu Leu Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser			
65	70	75	80
Pro Ile Asn Met Leu Tyr Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly			
85	90	95	
Lys Ile Pro Ala Met Val Val Asp Arg Cys Gly Cys Ser			

100

105

<210> 17
<211> 109
<212> PRT
<213> Artificial sequence

<220>
<221> MUTAGEN
<222> (83)..(97)
<223> Tetanus toxoid P2 epitope (SEQ ID NO: 13)

<220>
<221> SIMILAR
<222> (1)..(82)
<223> Identical to residues 267-348 in SEQ ID NO: 1

<220>
<221> SIMILAR
<222> (98)..(109)
<223> Identical to residues 364-375 in SEQ ID NO: 1

<220>
<221> SITE
<222> (73)
<223> Cys or Ser

<220>
<221> SITE
<222> (90)..(91)
<223> Lys Glu or Glu Gly

<400> 17
Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys
1 5 10 15
Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile
20 25 30
Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu
35 40 45
Phe Val Phe Leu Gln Lys Tyr Pro His Thr His Leu Val His Gln Ala
50 55 60
Asn Pro Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser
65 70 75 80
Pro Ile Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu
85 90 95
Leu Ile Pro Ala Met Val Val Asp Arg Cys Gly Cys Ser
100 105

<210> 18
<211> 109
<212> PRT
<213> Artificial sequence

<220>
<221> MUTAGEN

<222> (21)..(41)
<223> Tetanus toxoid P30 epitope (SEQ ID NO: 14)

<220>
<221> SIMILAR
<222> (42)..(109)
<223> Identical to residues 307-375 in SEQ ID NO: 1

<220>
<221> SIMILAR
<222> (42)..(109)
<223> Identical to residues 308-375 in SEQ ID NO: 1

<220>
<221> SITE
<222> (73)
<223> Cys or Ser

<220>
<221> SITE
<222> (90)..(91)
<223> Lys Glu or Glu Gly

<400> 18

Asp	Phe	Gly	Leu	Asp	Cys	Asp	Glu	His	Ser	Thr	Glu	Ser	Arg	Cys	Cys
1				5				10					15		
Arg	Tyr	Pro	Leu	Phe	Asn	Asn	Phe	Thr	Val	Ser	Phe	Trp	Leu	Arg	Val
								20		25			30		
Pro	Lys	Val	Ser	Ala	Ser	His	Leu	Glu	Tyr	Cys	Ser	Gly	Glu	Cys	Glu
								35		40			45		
Phe	Val	Phe	Leu	Gln	Lys	Tyr	Pro	His	Thr	His	Leu	Val	His	Gln	Ala
								50		55			60		
Asn	Pro	Arg	Gly	Ser	Ala	Gly	Pro	Cys	Cys	Thr	Pro	Thr	Lys	Met	Ser
								65		70		75		80	
Pro	Ile	Asn	Met	Leu	Tyr	Phe	Asn	Gly	Lys	Glu	Gln	Ile	Ile	Tyr	Gly
								85		90			95		
Lys	Ile	Pro	Ala	Met	Val	Val	Asp	Arg	Cys	Gly	Cys	Ser			
								100		105					

<210> 19
<211> 109
<212> PRT
<213> Artificial sequence

<220>
<221> MUTAGEN
<222> (49)..(69)
<223> Tetanus toxoid P30 epitope (SEQ ID NO: 14)

<220>
<221> SIMILAR
<222> (1)..(48)
<223> Identical to residues 267-314 in SEQ ID NO: 1

<220>
<221> SIMILAR

<222> (70)..(109)
<223> Identical to residues 336-375 in SEQ ID NO: 1

<220>
<221> SITE
<222> (73)
<223> Cys or Ser

<220>
<221> SITE
<222> (90)..(91)
<223> Lys Glu or Glu Gly

<400> 19
Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys
1 5 10 15
Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile
20 25 30
Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu
35 40 45
Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser
50 55 60
Ala Ser His Leu Glu Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser
65 70 75 80
Pro Ile Asn Met Leu Tyr Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly
85 90 95
Lys Ile Pro Ala Met Val Val Asp Arg Cys Gly Cys Ser
100 105

<210> 20
<211> 109
<212> PRT
<213> Artificial sequence

<220>
<221> MUTAGEN
<222> (79)..(99)
<223> Tetanus toxoid P30 epitope (SEQ ID NO: 14)

<220>
<221> SIMILAR
<222> (1)..(78)
<223> Identical to residues 267-345 in SEQ ID NO: 1

<220>
<221> SIMILAR
<222> (100)..(109)
<223> Identical to residues 366-375 in SEQ ID NO: 1

<220>
<221> SITE
<222> (73)
<223> Cys or Ser

<220>
<221> SITE

<222> (90)..(91)

<223> Lys Glu or Glu Gly

<400> 20

Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys
1 5 10 15

Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile
20 25 30

Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu
35 40 45

Phe Val Phe Leu Gln Lys Tyr Pro His Thr His Leu Val His Gln Ala
50 55 60

Asn Pro Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr Lys Phe Asn
65 70 75 80

Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala Ser
85 90 95

His Leu Glu Ala Met Val Val Asp Arg Cys Gly Cys Ser
100 105

<210> 21

<211> 109

<212> PRT

<213> Artificial sequence

<220>

<221> MUTAGEN

<222> (84)..(104)

<223> Tetanus toxoid P30 epitope (SEQ ID NO: 14)

<220>

<221> SIMILAR

<222> (1)..(83)

<223> Identical to residues 267-349 in SEQ ID NO: 1

<220>

<221> SIMILAR

<222> (105)..(109)

<223> Identical to residues 371-375 in SEQ ID NO: 1

<220>

<221> SITE

<222> (73)

<223> Cys or Ser

<220>

<221> SITE

<222> (90)..(91)

<223> Lys Glu or Glu Gly

<400> 21

Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys
1 5 10 15

Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile
20 25 30

Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu
35 40 45

Phe Val Phe Leu Gln Lys Tyr Pro His Thr His Leu Val His Gln Ala
50 55 60
Asn Pro Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser
65 70 75 80
Pro Ile Asn Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro
85 90 95
Lys Val Ser Ala Ser His Leu Glu Arg Cys Gly Cys Ser
100 105

<210> 22
<211> 254
<212> PRT
<213> Artificial sequence

<220>
<221> SIMILAR
<222> (110)..(124)
<223> Tetanus toxoid P2 epitope (SEQ ID NO: 13)

<220>
<221> SIMILAR
<222> (125)..(145)
<223> Diphtheria toxoid P30 epitope (SEQ ID NO: 14)

<220>
<221> SIMILAR
<222> (1)..(109)
<223> 109 C-terminal residues of human and bovine GDF-8
(residues 267-375 in SEQ ID NO: 1)

<220>
<221> SIMILAR
<222> (146)..(254)
<223> 109 C-terminal residues of human and bovine GDF-8
(residues 267-375 in SEQ ID NO: 1)

<220>
<221> SITE
<222> (90)..(91)
<223> Lys Glu or Glu Gly

<220>
<221> SITE
<222> (235)..(236)
<223> Identical to (90)..(91)

<400> 22
Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys
1 5 10 15
Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile
20 25 30
Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu
35 40 45
Phe Val Phe Leu Gln Lys Tyr Pro His Thr His Leu Val His Gln Ala
50 55 60
Asn Pro Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser

65	70	75	80
Pro Ile Asn Met	Leu Tyr Phe Asn Gly Lys	Glu Gln Ile Ile Tyr	Gly
85	90	95	
Lys Ile Pro Ala Met Val Val Asp Arg Cys	Gly Cys Ser Gln Tyr Ile		
100	105	110	
Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu	Phe Asn Asn Phe		
115	120	125	
Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val	Ser Ala Ser His Leu		
130	135	140	
Glu Asp Phe Gly Leu Asp Cys Asp Glu His	Ser Thr Glu Ser Arg Cys		
145	150	155	160
Cys Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala	Phe Gly Trp Asp Trp		
165	170	175	
Ile Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys	Ser Gly Glu Cys		
180	185	190	
Glu Phe Val Phe Leu Gln Lys	Tyr Pro His Thr His Leu Val His Gln		
195	200	205	
Ala Asn Pro Arg Gly Ser Ala Gly Pro Cys Cys	Thr Pro Thr Lys Met		
210	215	220	
Ser Pro Ile Asn Met Leu Tyr Phe Asn Gly Lys	Glu Gln Ile Ile Tyr		
225	230	235	240
Gly Lys Ile Pro Ala Met Val Val Asp Arg Cys	Gly Cys Ser		
245	250		

<210> 23

<211> 160

<212> PRT

<213> Artificial sequence

<220>

<221> MUTAGEN

<222> (16)..(36)

<223> Tetanus toxoid P30 epitope (SEQ ID NO: 14)

<220>

<221> MUTAGEN

<222> (37)..(51)

<223> Tetanus toxoid P2 epitope (SEQ ID NO: 13)

<220>

<221> SIMILAR

<222> (1)..(15)

<223> Identical to residues 216-230 of SEQ ID NO: 1

<220>

<221> SIMILAR

<222> (52)..(160)

<223> Identical to residues 267-375 of SEQ ID NO: 1

<220>

<221> SITE

<222> (124)

<223> Cys or Ser

<220>

<221> SITE

<222> (141)..(142)
<223> Lys Glu or Glu Gly

<400> 23

Leu Lys Gln Pro Glu Ser Asn Leu Gly Ile Glu Ile Lys Ala Leu Phe
1 5 10 15
Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala
20 25 30
Ser His Leu Glu Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile
35 40 45
Thr Glu Leu Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser
50 55 60
Arg Cys Cys Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala Phe Gly Trp
65 70 75 80
Asp Trp Ile Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly
85 90 95
Glu Cys Glu Phe Val Phe Leu Gln Lys Tyr Pro His Thr His Leu Val
100 105 110
His Gln Ala Asn Pro Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr
115 120 125
Lys Met Ser Pro Ile Asn Met Leu Tyr Phe Asn Gly Lys Glu Gln Ile
130 135 140
Ile Tyr Gly Lys Ile Pro Ala Met Val Val Asp Arg Cys Gly Cys Ser
145 150 155 160

<210> 24

<211> 13

<212> PRT

<213> Unknown

<220>

<223> PADRE Peptide

<400> 24

Ala Lys Phe Val Ala Ala Trp Thr Leu Lys Ala Ala Ala
1 5 10